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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-q9y4x1.res made by jdelaval on Sun 2 Sep 101 10:48:09-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File: q9y4x1.pap

100-
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
S -
E 5-
O -
U -
E -
N -
C -
E -
S 0-
SCORE 0 1 1 2 2 3 3 4 4 5
STDV

PARAMETERS

Similarity matrix Unitary K-tuple 2
Translation Frame 6
Mismatch penalty 1 Joining penalty 20
Gap penalty 1.00 Window size 32
Gap size penalty 0.05
Cutoff score 1
Randomization group 0

SEARCH STATISTICS

Scores: Mean 5 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 527
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
1. q9y4x1	UDP GLUCURONOSYLTRANSFERASE (527	5	89	0.00	1

1. US-09-784-340-1 (1-2759)
q9y4x1 UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: q9y4x1 check: 7657 from: 1 to: 527

ID Q9Y4X1 PRELIMINARY; PRT; 527 AA.
AC Q9Y4X1;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-OLEFACTORY;
RX MEDLINE=99289328; PubMed=10359671;
RA Jeditlschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase."
RL Biochem. J 340:837-843(1999).
DR EMBL: AJ006054; CAB41974.1;
DR InterPro: IPR002213;
DR Pfam: PF00201; UDPGT: 1.
DR PROSITE: PS00375; UDPGT: 1.
KW transferase; Glycosyltransferase.
SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A21F17 CRC64;

q9y4x1 length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..

Initial Score = 5 Optimized Score = 89 Significance = 0.00
Residue Identity = 19% Matches = 112 Mismatches = 336
Gaps = 117 Conservative Substitutions = 0
Translation Frame= 1

QPLQISVXGNCHEVXQVSGISAPALLCWLMWSPGVALXHEPLACQGHSHRAHSEKXGNSIDSL-
10 20 30 40 50 60 70
MUNLLFSLQI--SLIGTTIGNVLIIMPEGSS---HMLNVKTIIDELI
KAFVN---XLOEAFCEIEXGPRAT-----GQNRKKXNXCPSSECLALINLAISYKIKKFFCANRR
80 90 100 110 120 130
KKEHNVTVLVASGALFTTPSPNSPLTEIYKVPFGKERIEGVKIDFVS---TWLENNPSSFTIMRYQEMAK
50 60 70 80 90 100 110
NFKNDVXELYLQSDAYEEATGNG-----LRCNATRPDGS-LMRPDG-XVA---CSPFCATXNFCRQYQAK
140 150 160 170 180 190
VIRDFHWVSOEICD--GVLRNOOLMAKLRKSKFEVLVSDVPFGGDIVALKGIPE---MYSLRFSFA-
120 130 140 150 160 170
LWETSSFTLCATGAYDTRNQNNDLSGSKSKFNAPFVPLDLSGL--RLSPLGR-VLXGGRKRAHYIMXDCGK
200 210 220 230 240 250 260
-----STVERKHC-----GK--VPPSPYPAVALSETLQDMSFTDRIRNFISYHLQDYMFETLWK
180 190 200 210 220
SXDMANNTIIIGFXISSTIIPYXLYCQWALXATCQSF-----AKGNGKFCPEF--RGRW
270 280 290 300 310
SMDSYSKALGRPTTLCETMGKAEIWLIRTYWDFEPPRYLPNFEFVGLGCKPAKPLPREMEEFIQSSGKN

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-q9y4x1.res made by jdelaval on Sun 2 Sep 101 10:48:29-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File : q9y4x1.pep

100-
N -
U 50-
M -
B -
E -
R -
O -
F 10-
S -
Q 5-
E -
U -
N -
C -
E -
S 0-
SCORE 0 1 2 3 4 5 6 7
STDEV

PARAMETERS
Similarity matrix Unitary K-tuple 2
Translation Frame 6
Mismatch penalty 1 Joining penalty 20
Gap size penalty 1.00 Window size 32
Cutoff score 0.05
Randomization group 1
0

SEARCH STATISTICS
Scores: Mean 7 Median 0 Standard Deviation 0.00
Times: CPU 00:00:00.00 Total Elapsed 00:00:00.00
Number of residues: 527
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.
A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sign.	Frame
1. q9y4x1	UDP GLUCURONOSYLTRANSFERASE (527	7	81	0.00	3

1. US-09-784-340-1 (1-2759)
q9y4x1 UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: q9y4x1 check: 7657 from: 1 to: 527

ID 09Y4X1 PRELIMINARY; PRT: 527 AA.
AC 09Y4X1;
DT 01-NOV-1999 (TEMBLrel. 12, Created)
DT 01-NOV-1999 (TEMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFACTORY;
RX MEDLINE=9289328; PubMed=10359671;
RA Jeditschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase.";
RL Biochem. J 340:837-843(1999).
DR EMBL; AJ006054; CAB41974.1;
DR InterPro; IPR002213;
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A421F17 CRC64;

q9y4x1 Length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..
Initial Score = 7 Optimized Score = 81 Significance = 0.00
Residue Identity = 18% Matches = 108 Mismatches = 377
Gaps = 109 Conservative Substitutions
Translation Frame= 3

TIADCVRELPSXGLTSLWYFCSSSVLAVDSVSKMCGPVYTAIGLMSRSPFKSSXXEAMRXQYXITQS
80 90 100 110 120 130 140
LRKLTGSLHKNLRLMSICHRTEQKKMYLTYLXMKSCAYOPGQNLXNMTFLKXELKXKCVRLSTIR
150 160 170 180 190 200 X 210
RLKRSYRKPTTMXCLXTLFPVETXWLSCLOSILCSHLEFLKALIMSEAVGNFOLHFPYGLXODXOTEXP
MLNNL-----
X

220 230 240 250 260 270 280
FWKEXKIQCFQPCSTSGFRITTTIFGKSFIVRHXEGPLHYRLMEKRLRYGXEHGILNLFNHTNLTLS--L
-----LFLSLQISLIGTLGVL--WPMEG---SHMLNVR--IIIDELI--KKHNVTVLVASGAL
10 20 30 40 50
290 300 310 320 330 340
LEDCTVVLKLCIKRWK---ILSRVGSKWLVCFMGCHCFKMLQKRLSLILO-----PLPRSHRRCYG
FIPPTSN-PSLTFEIVKVPQKEKIEG--VIKDFVSTWLENRSPSTIMRFYQEMAKVTKDFHVSQELCDG
60 70 80 90 100 110 120
350 360 370 380 390 400 410
GTR-----EKNHPIKXEPILCGMIGYR--RMIFLIVIPKPLSLIMVEXGSMKLTGSGSLMWERPY--LVISL

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VLKNOQIMAKLKSKFEVLVSDPVPCGDIVALKLGIPMYSL-RFSPASTVEKHGKVPYPPSVPAVLSE
130 140 150 160 170 180 190
IT---XLTFRFEDLKXKTKSLKQAKIYXGL--XEOSLPILIKR--MLXDYOETMINL--XSPXIEQSSG
LTDQMSFDR---IRNFISYHLDYMEFTLMKSWDSYYSKALGPTTLCMGCAEIMLIRTYWDEFEPFPP
200 210 220 230 240 250 260
480 490 500 510 520 530 540
SSLSGATKEPSTC---DQLP--WTSPPSSTLLMXKLGSCXPMOLLVSCSONVEFPVKNLKLRKRGNR
YLPNFEFGJHCHGPAKLPKPEMEEFIS-----SGKNGVVVSIGS-----MKNLTEKANLIASA
270 280 290 300 310 320
550 560 570 580 590 600
SFQI-QEPPDVIILLIPATXNLVTLF-----STYLFYFILAIKPRIPKXGGEVISEFRCTPLGLTLF
LAQIPQKVLKMRKGRKRPAT-LGNTQOLFDMIPONDIGHPKTKAFITHGNGIYEAI-YHGVPWGVPMFA
330 340 350 360 370 380 390
610 620 630 640 650 660 670
SHEVYQGEHYIXIFLELISLFPKRYHESNLKXGDLQYADSMCLHKHMDVKKXKXNSQNSVNHQNXSLX
DQPDNIAMKAKGAVEYNL-----NTMTSYDLISA---LRTVINEPSYKENAMRLSRHHQPVKPL
400 410 420 430 440 450
680 690 700 710 720 730 740 750
HXLVNSNIMITFLFOFKALLHTOHXSQTMNCXKXKXGITLRYCYISTYLIKMSXPTFLPSLNKHFLCVID
DRAV--FWIEFVMRHKGAKHLRVAAHDLTWFOYHSLDIVIGFLVC--VTTAIFLVIQCCLFSCQKFGKGRK
460 470 480 490 500 510 520
X 760 770 780 790 800 810 820
DKXYVLIVLKKXKKLKFSTIEKMSIRTSKTDYFEISNHKKYVIVISDFIKFLIYHLIKMSILXNDEYSX
KKRE
X
830 840 850 860 870 880 890
FLSLKSKYXFTVERKRDACSESKKKKKKNTWMLPLRSVSLTAHCAVYTHIYDSDTWMLPLRSVSLTALSCVVS
900 910
VSLFALSCRYVAYRXQONTVSRYVA

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FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-q9y4xl.res made by jdelaval on Sun 2 Sep 101 10:48:38-PDT.

Query sequence being compared: US-09-784-340-1 (1-2759)
Number of sequences searched: 1
Number of scores above cutoff: 1

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
file : q9y4xl.pep

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100-
N -
U -
M -
B -
E -
R -
O -
F 10-
S -
E 5-
O -
U -
E -
N -
C -
E -
S 0-
SCORE 0 1 1 2 3 3 4 5 5 6
STDEV

```

PARAMETERS

Similarity matrix	Unitary	K-tuple	2
Translation frame	6		
Mismatch penalty	1	Joining penalty	20
Gap penalty	1.00	Window size	32
Gap size penalty	0.05		
Cutoff score	1		
Randomization group	0		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
	6	0	0.00
Times:	CPU		
	00:00:00.00		
Number of residues:	527		
Number of sequences searched:	1		
Number of scores above cutoff:	1		
		Total Elapsed	
		00:00:00.00	

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found.

The list of best scores is:

Sequence Name	Description	Length	Score	Opt.	Sig.	Frame
1. g9y4xl	UDP GLUCURONOSYLTRANSFERASE (527	6	89	0.00	4

1. US-09-784-340-1 (1-2759)
g9y4xl UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: g9y4xl check: 7657 from: 1 to: 527

ID 09y4xl PRELIMINARY; PRT; 527 AA.
AC 09y4xl.
DT 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFATORY;
RX MEDLINE=9289328; PubMed=10359671;
RA Jellitschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase.";
RL Biochem. J. 340:83-843(1999).
DR EMBL; AJ006054; CAB41974.1; .
DR InterPro; IPR002213; .
DR Pfam; PF00201; UDPGT; 1.
DR PROSITE; PS00375; UDPGT; 1.
KW Transferase; Glycosyltransferase.
SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A421F17 CRC64;

09y4xl length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..

Initial Score = 6 Optimized Score = 89 Significance = 0.00
Residue Identity = 20% Matches = 119 Mismatches = 360
Gaps = 116 Conservative Substitutions = 0
Translation Frame= 4

```

RYVTADSVLLSTIRYVTAQCCORRYARNAXQCCORVATXRHDSYAVNDMLRNGMTVCCORATXRHDSVFF
      10      20      30      40      50      60      70
      80      90     100     110     120     130     140
FFFTFRSISLFFYSKLYFLKRXELAVFIILKNRHLNOYYOLKFKIRNYNHLIFLMTYLKILCLTXISY
150 160 170 180 190 200 210
GHFLYVRKFOFLLEFDNNKNCLEFIITNTQMSYKWKQCKRLHLDVCGNIAMISCNALSSFLAIHCLRS
220 230 240 250 260 270 280
VMLGKXKGLFLLKKKNHVTNKLMSKNASLICYVYXILKILHFLLYIHVFYQTPGISILQVTL--SLKVR
      20      30      40      50      60      70
LIGTLGNGVLIWPMEGSHMLNVKLIIDELIKKEHNVTVLVASSGALFTTPRS--NPSL-----FEIYKV
290 300 310 320 330 340 350
EVMT-----SMKQYQKXENLDVEMSLCHKVRRESKHTXENATREXDLITTSXSMNSRLYSXDKITEYLKK
      10      20      30      40      50      60      70
LIGTLGNGVLIWPMEGSHMLNVKLIIDELIKKEHNVTVLVASSGALFTTPRS--NPSL-----FEIYKV
360 370 380 390 400
XOGFHOILCGMNKXDYPIRSF--LNLIE-RSIPSFLSFXFY-----XIFDKIKINILKTRIXO
      10      20      30      40      50      60      70
PGKGERI-----EGVTKDFSTVLENRPSPS-TIMRFYQEMAKVIKDFHNVSOEIDGVILKN-----QO
      80      90     100     110     120     130

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410 420 430 440 450 460 470
LPHRSAGTQSHLXSSAGTRXGHGQILGAMILGAGANQTSRRLLDGLALQVDHGEFLIISXSLYKRNRRXL
      10      20      30      40      50      60      70
LMAKLKSKFEVLVS-DPVFPCGDIVA---LKLGIPEMYS--LRSPASTVEKKHCKGVPPSYVAVVSEL
140 150 160 170 180 190 200
TDQMSFTDRIIRNFISYHLQDMETLMKSWDSYSKALGRPTLCEMGAEIWLIRTYWDFEFPFRPL-
      210      220      230      240      250      260
480 490 500 510 520 530 540
FSKPSVNLRLSKFXSLFLQ-----LLMPSCELCY-QADHQIMEL-PPXGPHGKXLR-SHSFHHXXKLMFW
      10      20      30      40      50      60      70
DDQEDHSGVSNHTAEVYLLMMVFEICTSITPSVSGGGLKQXHPFLAHFETVPER-----TPQ
550 560 570 580 590 600
PNFEFVGLHCKPA-KPLPKMEEF-----IQSSGKNG-----VVFSLGSMVKNLFEKANLIASALAIPO
270 280 290 300 310 320 330
YHLPLNSGQNFPPFXAKLMQVYSAILQ---QTSXGVMEIEIONPMFEVLAISQLFQSHIMXMAFLMPYK
610 620 630 640 650 660 670
KVLNRYKG-KKPAIILGNNTOLFDMITPONDILGHKTKAFITHGSGTNGIYEAIYHGVF-----MGVPMFA
340 350 360 370 380 390
680 690 700 710 720 730 740
TLPKNDSNPESRSQTKLALNLFLLFPERFCLLVLSXQVHRVVELEVSHSPAYCLLOKFXVXAKGL-Q
      10      20      30      40      50      60      70
DOEDN-----IAHMKAGAIVEVNLNMTSYDL-----SALRTVINPEPSYKENAMRLSRITHNDQPVKIDR
400 410 420 430 440 450
750 760 770 780 790 800 810
ATQPSGLHRESQGLALHRSWFPAASSYASDCRXSSHTS--FLKFLFQCKNHLILKILANLISLARHSELG
      10      20      30      40      50      60      70
AVFWLEFVWRHKG-AKH---LRVA---AHDLTWFQYHSLDVLGFLVCVTTAIFLVYIQCCLFSCQKFGKIG
460 470 480 490 500 510 520
820 X 830 840 850 860 870 880
QQIFHFLFCFPAVAYPPQISIMOKASCQITKALSESILLPHGLSLXALLKEXPXKANGSCHRATPGLSHRH
      10      20      30      40      50      60      70
KKKKRE
890 900 910
SOHRRRAGAEIRKLCIQTSXWQFPHTLIGN

```


[illegible]

IntelIGenetics

FastDB - Fast Pairwise Comparison of Sequences
Release 5.4

Results file 09-784340-1-q9y4x1.res made by jdelaval on Sun 2 Sep 10 10:48:53-PDT.

```
Query sequence being compared:US-09-784-340-1 (1-275)
Number of sequences searched: 1
Number of scores above cutoff: 1
```

Results of the initial comparison of US-09-784-340-1 (1-2759) with:
File : q9y4xl.pcp

	100	-
N	-	
U	-	
M	50	-
B	-	
E	-	
R	-	
O	-	
F	10	-
S	-	
E	5	-
O	-	
D	-	
E	-	
N	-	
C	-	
E	-	
S	0	-
SCORE	0	-
STDEV	1	-
	1	-
	2	-
	3	-
	3	-
	4	-
	5	-
	5	-
	6	*

	Unitary	K-tuple
Similarity matrix	6	2
Translation frame	1	20
Mismatch penalty	1.00	Window size
Gap penalty	0.05	32
Gap size penalty	1	
Cutoff score	0	
Randomization group		

SEARCH STATISTICS

Scores:	Mean	Median	Standard Deviation
5	5	0	0.00

Times:	CPU	Total Elapsed
	00.00.00.00	00.00.00.00

Number of residues: 527
Number of sequences searched: 1
Number of scores above cutoff: 1

The scores below are sorted by initial score.
Significance is calculated based on initial score.

A 100% identical sequence to the query sequence was not found

The list of best scores is:

Sequence Name	Description	Length	Score	Opt. Frame
1. q9y4xl	UDP GLUCURONOSYLTRANSFERASE (527	6	83 0.00 6

1. US-09-784-340-1 (1-2759)
q9y4xl UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).

TOIG of: q9y4xl check: 7657 from: 1 to: 527

ID Q9Y4X1 PRELIMINARY; PRT; 527 AA.
AC Q9Y4X1;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE UDP GLUCURONOSYLTRANSFERASE (EC 2.4.1.17).
GN UGT2A1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OLFATORY;
RX MEDLINE=99289328; PubMed=10359671;
RA Ueditschky G.A., Cassidy A.J., Sales M., Pratt N., Burchell B.;
RT "Cloning and characterization of a novel human olfactory UDP-
glucuronosyltransferase."
RL Biochem. J 340:837-843(1999).
DR EMBL: AJ006054; CAB41974.1; .
DR InterPro: IPR002213; .
DR Pfam: PF00201; UDPGT; 1.
DR PROSITE: PS00375; UDPGT; 1.
KM Transferase; Glycosyltransferase.
SQ SEQUENCE 527 AA; 59872 MW; B99E73AA9A421F17 CRC64;

Q9Y4X1 Length: 527 September 1, 2001 09:58 Type: P Check: 7657 ..

Initial Score = 6 Optimized Score = 83 Significance = 0.00
Residue Identity = 19% Matches = 116 Mismatches = 333
Gaps = 150 Conservative Substitutions = 0
Translation Frame= 6

LRNGXQCFVAVNDTLRNGMTVLSTIRSKRMVLTSLIRVYTAQCRCQRYATXRHDSGLSTIRVYTAQCFFEF
80 90 100 110 120 130 140
FFYQNKRLFFLQXIIILIEIRIMSIHFKKXFKSSVLSIKILXNQKLOSHSNGYLSQNNLNFNLILM
MLNLL
X

150 160 170 180 190 200 210
TFSLCKRTSVSFIIXGXQXELSIYHOETKRNVSXMAEMXAMTSKXGMKYS-KLFXVXCPVIVFSN-SL-S
LFSL-QISLIGTLGGLVNLWPEGSHWLNKIIIDELIKKEHNVTYLVASGALF-----TTPTSNPSLTP
10 20 30 40 50 60 70

220 230 240 250 260 270
ET-----SNAGVEGLI-----XTEKES-----LCYSXQANVIECFIDGLNLFVFTFTSLHPVCAN
EIIKVPFGKRIEGLVNDPFTWLENRPSTIMRFYQEMAKVILDF-----HNVSOELCDGYL
80 90 100 110 120 130

280 290 300 310 320
TRNQHIGHPITTXGRSDVMEIVISELGRFC--IHYL-----VSOSERREXA-----HLGKCNEMRY--
KNQOLMA-----KLKSKFEVLVS-DPVPCGDYALKLGIIPMWSLRSPASTVEKHGCKVPPSYVP
140 150 160 170 180 190

330 340 350 360 370 380 390
--THNLMIMEFFXALIXLRXNRI-----DNM-KIARESPNBMLELGLPQVLEFGKITSLFVLVLN
AVLSELDQMSF---TRIRNFYTHADYVFEFLMKSMDSYSKALGRPTTLOETGK-----AEIWLIRY
200 210 220 230 240 250

400 410 420 430 440 450
FXQENKHFVFNKNIATVATQVSRNPITSIEXCWQNRVSWAADRCLAPL-WMTNSIO---KTARSRGFTGS
WDPE-----FPRPLPNFEFVGLHCKPA-----KLPRKMEEFIOSSGNGVVSIGSM
260 270 280 290 300 310

460 470 480 490 500 510
WXIL-----DNLIAFSL--XEEVMTVLKALSSSL-----VIYKFIPTAFLAFMXAMLSXSP
VKNLTEKANILIASALAOIPQKVLMMRKKGKRPALGNTOLEFDWIPONDLLGHKTKAFLTHGNTGNEYAI
320 330 340 350 360 370 380

520 530 540 550 560 570 580
NMGPTIGTPMXIASXIPFIPPYVYK-ALVYLGXPRRSFMCIOYSRVLPVNDGFFPYLYLHNTFCIIMARAE
YHGVPNGVP-MFADQPDNLTMMAKGAAY---EVNLNTMTSVLDLSALRTVYNEPSYKEN-----
390 400 410 420 430

590 600 610 620 630 640
AMIL-----AFSSVTFXNSDPRENTTIPSPELMTKFSISLGLKALAGLCNPNPTNSKLGWYX
AMRISRIHNDOPVPLDRAVWVIEFVNRHKGAKHLRVAADHDTWFOYHSLDVLGFLVLC-VTFAIFLVIOCC
440 450 460 470 480 490 500 510

650 660 670 680 690 700 710
GNSKQYVRISHISAFPTVSHNVGLPINALNNSQXXSXIXIQKNKTESIEFFTLRSKVLVSVPIGT
LFSQCKRGKIGKKKRE
520 X

720 730 740 750 760 770 780
GTXSAGSFPQLSILIPTEILSVSTKGTASNSAIRSPQGITGSISITSXLVSCSFFISVXLIKLSHILF

790 800 810 820 830 840 850
KVPILSTIKKSPNFTTDCQVDRPGKTFPARSTNISFSSVLSGCIWTTTSNFMNAGLXISNEGFEAVNTVTSMP
860 870 880 890 900 910
LTMSSRMTLTLSQLMSQGHTRFPQNPQPTOKSCRSRNTKADLSDLMAVPSHTDLQW

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